

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
METHODS PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Brown, Martin, Haller & McClain
(B) STREET: 1660 Union Street
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 6869-402A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-238-0999
(B) TELEFAX: 619-238-0062
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

0009648.051298

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTT	AGTTTTCTC	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTTCGTCA	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTTAAT	TTTCCACCTT	TTCATTTTTT	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTT	ACTGATTTTC	TCATTTTTTCA	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AAATTTTCAA	CTTTTTCAAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTTCAGT	TTTTTCAGTGA	TTTCGTCAAT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTTT	CTTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTT	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTT	ACGTTTTTCA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACAG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCAGTT	TTTCAGTGAA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTGT	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTTCGTTG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTTCC	AGAACTTCTT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720

AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGTT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCCAGA	ATCTTGTTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTAAAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCAAC	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACCTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTTC	1920

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GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAAGTATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340
CCGTCACACC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCCAT	CTGCCCCGAG	GTGGCGGCTG	2400
CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

00096648-061290

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CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

27

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

GTC ACA AAC AGT GCA CCT ACT 69
Val Thr Asn Ser Ala Pro Thr

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942
(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35				40						45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55				60						
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70				75					80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90					95		

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TTA Leu	CTT Leu	GAT Asp	CAT His 100	TAC Tyr	AAA Lys	TAT Tyr	CTT Leu	ACT Thr 105	GCA Ala	TGG Trp	TTG Leu	AAC Asn	TTC Phe 110	TTA Leu	ATT Ile	336
TAC Tyr	CAA Gln	AGA Arg 115	AGA Arg	TCA Ser	TTT Phe	TTT Phe	GTC Val 120	GGC Gly	CAT His	GAT Asp	TGG Trp	GGT Gly 125	GCT Ala	TGT Cys	TTG Leu	384
GCA Ala	TTT Phe 130	CAT His	TAT Tyr	AGC Ser	TAT Tyr	GAG Glu 135	CAT His	CAA Gln	GAT Asp	AAG Lys	ATC Ile 140	AAA Lys	GCA Ala	ATA Ile	GTT Val	432
CAC His 145	GCT Ala	GAA Glu	AGT Ser	GTA Val	GTA Val 150	GAT Asp	GTG Val	ATT Ile	GAA Glu	TCA Ser 155	TGG Trp	GAT Asp	GAA Glu	TGG Trp	CCT Pro 160	480
GAT Asp	ATT Ile	GAA Glu	GAA Glu	GAT Asp 165	ATT Ile	GCG Ala	TTG Leu	ATC Ile 170	AAA Lys 170	TCT Ser	GAA Glu	GAA Glu	GGA Gly	GAA Glu 175	AAA Lys	528
ATG Met	GTT Val	TTG Leu	GAG Glu 180	AAT Asn	AAC Asn	TTC Phe	TTC Phe	GTG Val 185	GAA Glu	ACC Thr	ATG Met	TTG Leu	CCA Pro 190	TCA Ser	AAA Lys	576
ATC Ile	ATG Met	AGA Arg 195	AAG Lys	TTA Leu	GAA Glu	CCA Pro	GAA Glu 200	GAA Glu	TTT Phe	GCA Ala	GCA Ala	TAT Tyr 205	CTT Leu	GAA Glu	CCA Pro	624
TTC Phe	AAA Lys 210	GAG Glu	AAA Lys	GGT Gly	GAA Glu	GTT Val 215	CGT Arg	CGT Arg	CCA Pro	ACA Thr	TTA Leu 220	TCA Ser	TGG Trp	CCT Pro	CGT Arg	672
GAA Glu 225	ATC Ile	CCG Pro	TTA Leu	GTA Val	AAA Lys 230	GGT Gly	GGT Gly	AAA Lys	CCT Pro	GAC Asp 235	GTT Val	GTA Val	CAA Gln	ATT Ile	GTT Val 240	720
AGG Arg	AAT Asn	TAT Tyr	AAT Asn	GCT Ala 245	TAT Tyr	CTA Leu	CGT Arg	GCA Ala	AGT Ser 250	GAT Asp	GAT Asp	TTA Leu	CCA Pro	AAA Lys 255	ATG Met	768
TTT Phe	ATT Ile	GAA Glu	TCG Ser 260	GAT Asp	CCA Pro	GGA Gly	TTC Phe	TTT Phe 265	TCC Ser	AAT Asn	GCT Ala	ATT Ile	GTT Val 270	GAA Glu	GGC Gly	816
GCC Ala	AAG Lys	AAG Lys 275	TTT Phe	CCT Pro	AAT Asn	ACT Thr	GAA Glu 280	TTT Phe	GTC Val	AAA Lys	GTA Val	AAA Lys 285	GGT Gly	CTT Leu	CAT His	864
TTT Phe	TCG Ser 290	CAA Gln	GAA Glu	GAT Asp	GCA Ala	CCT Pro 295	GAT Asp	GAA Glu	ATG Met	GGA Gly	AAA Lys 300	TAT Tyr	ATC Ile	AAA Lys	TCG Ser	912
TTC Phe 305	GTT Val	GAG Glu	CGA Arg	GTT Val	CTC Leu 310	AAA Lys	AAT Asn	GAA Glu	CAA Gln	TAA						945

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC

30

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852755" 84956060